

To be assigned; Group Art Unit: To be assigned
 1488.1280006/EKS/EJH;
 Venues: Wei et al.; Tel: 202/371-2600
 title: Tumor Necrosis Factor Receptor 5

CCTCTCCACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGGAGTTGACCAG
 AGATGCAAGGGGTGAAGGAGCGCTTCTACCGTTAGGAACTCTGGGGACAGAGCGCCCC
 GGCGCCTGATGGCCGAGGCAGGGTGCAGCCAGGACCCAGGACGGACGGCGTCGGGAACCATA
 CCATGGCCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCGGTCTGCTGC
 M A R I P K T L K F V V V I V A V L L P
 CAGTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTCCCCAGCAGACAGTGG
V L A Y S A T T A R Q E E V P Q Q T V A
 CCCCACAGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGAT
 P Q Q Q R H S F K G E E C P A G S H R S
 CAGAACATACTGGAGCCTGTAACCGTGACAGAGGGTGTGGATTACACCAACGCTTCCA
 E H T G A C N P C T E G V D Y T N A S N
 ACAATGAACCTTCTTGCTTCCATGTACAGTTGTAATCAGATCAAAACATAAAAGTT
 N E P S C F P C T V C K S D Q K H K S S
 CCTGCACCATGACCAGAGACACAGTGTGTCACTGTAAAGAAGGCACCTTCCGGAATGAAA
 C T M T R D T V C Q C K E G T F R N E N
 ACTCCCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTA
 S P E M C R K C S R C P S G E V Q V S N
 ATTGTACGTCTGGGATGATATCCAGTGTGTGAAGAATTGGTGCCAATGCCACTGTGG
 C T S W D D I Q C V E E F G A N A T V E
 AAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCCCGGGACTCCTGCCAGCTGCTG
 T P A A E E T M N T S P G T P A P A A E
 AAGAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCA
 E T M N T S P G T P A P A A E E T M T T
 CCAGCCCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCAAGCCCCGGGACTC
 S P G T P A P A A E E T M T T S P G T P
 CTGCCAGCTGCTGAAGAGACAATGACCAAGCCCCGGGACTCCTGCCCTTCTCATT
 A P A A E E T M T T S P G T P A S S H Y

FIG.1A

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ACCTCTCATGCACCACATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTGTTT
L S C T I V G I I V L I V L L I V F V *

GAAAGACTTCACTGTGGAAGAAATTCTTCCTTACCTGAAAGGTTAGGTAGGCGCTGGC
TGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCCTCTGCTGTGTTCCCACAGAC
AGAAACGCCTGCCCTGCCCAAGTCCTGGTGTCCAGCCTGGCTCTATCTTCCTCCTT
GTGATCGTCCCACATCCCCACATCCCGTGCACCCCCCAGGACCCCTGGTCTCATCAGTCCCTC
TCCTGGAGCTGGGGTCCACACATCTCCAGCCAAGTCCAAGAGGCAGGGCAGTTCC
CCATCTTCAGGCCAGCCAGGCAGGGCAGTCGGCTCCTCAACTGGGTGACAAGGGTGA
GGATGAGAAGTGGTACGGGATTATTAGCCTGGTCAGAGCAGAACACAGAGATTTTC
CGTAAAAAAA

FIG. 1B

App. b. To be assigned; Group Art Unit: To be assigned
DKT. No. 1488.1280006/EKS/EJH;
Inventors: Wei *et al.*; Tel: 202/371-2600
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FIG. 2A

To be assigned; Group Art Unit: To be assigned
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 inventors: Wei *et al.*; Tel: 202/371-2600
 title: Tumor Necrosis Factor Receptor 5

		Consensus #1
39	- - K R D S V C P Q G K Y I H - -	P Q N N S I C C T K C H K G T Y L Y N D C P G T N F R 1
32	- - Y - A P E P G S T C R L R E Y D Q T A Q M C C S K C S P G Q H A K V F C - -	T N F R 2
34	- - T - - - - Y R I E N Q T C W D Q D K E Y Y E P M H D V C C S R C P P G E E F V F A V C - -	N G F R
36	- - E L R K T V T V E T Q N L E G L H H D G Q F C H K P C P P G E R K A R D C T V F A S	L T b R
36	- - E - - - - D R P F E D T C H G N P S H Y Y D K A V R R C C Y R C P M G L F P T Q Q C P Q C D 27	
29	- - D R P F E D T C H G N P S H Y Y D K A V R R C C Y R C P M G L F P T Q Q C P Q C D 30	
22	- - T R S L Q D P - - - - T R S L Q D P - - - -	C D 40
24	- - T R S L Q D P - - - - T R S L Q D P - - - -	
21	- - G - - - - D T Y P S N D R - C C H E C R P G N G M V S R C S R O X 40	4-1 B B
33	- - G - - - - D T Y P S N D R - C C H E C R P G N G M V S R C S R O X 40	
28	- - P N G K C K D T E Y K R H N - - - - L C C L S C P P G T Y A S R I L C D S V C 22	
26	- - S N G K C K D N E Y K R H H - - - - L C C L S C P P G T Y A S R I L C D S C R M B	
33	- - E V P Q Q T V A P Q - - - - Q Q R H S F K G E E C P A G S H R - - - -	T N F R - like

FIG. 2B

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		Consensus #1										Consensus #2																				
		TNFR1					TNFR2					NGFR					LILR															
		C		S			K		C			R		K			M			G		TNFR1										
		C		S			K		C			R		K			M			G		TNFR2										
		C		S			K		C			R		K			M			G		NGFR										
75	P	G	Q	D	T	C	R	-	E	C	E	S	G	S	-	F	T	A	S	E	N	H	L	R	C	T	N	F	R	I		
68	T	K	T	S	D	T	V	-	E	D	S	T	Y	T	Q	-	W	N	W	V	P	E	C	L	S	S	R	C	M	R	I	
60	N	Q	-	T	-	V	-	C	-	P	C	L	D	S	V	T	F	S	D	V	V	S	A	T	E	P	C	R	T	R		
73	S	R	S	Q	D	T	V	-	C	-	K	T	C	-	P	H	N	S	Y	E	H	W	N	H	L	S	T	T	R	R		
76	N	-	G	D	E	P	D	C	V	-	P	C	Q	E	G	K	Y	T	D	K	A	H	F	S	S	K	C	R	C			
56	H	R	K	A	-	A	Q	C	D	-	P	C	I	P	G	V	S	F	S	P	-	-	-	-	-	-	-	-	-	-		
R	-	-	P	T	D	C	R	K	Q	C	-	E	P	D	Y	Y	L	D	E	A	R	C	T	A	C	V	T	C	S			
R	-	T	E	F	T	E	T	E	T	E	C	-	G	E	S	E	F	L	D	T	W	N	R	E	T	H	C	H	Q			
61	T	E	F	N	Q	-	I	C	-	S	P	C	-	P	P	N	S	F	S	S	A	-	G	Q	R	T	C	D	I			
52	N	R	N	Q	-	V	-	V	-	C	R	-	P	C	-	G	P	G	F	Y	N	D	V	V	S	S	K	-	P	C		
40	S	Q	N	T	-	T	N	T	-	Q	C	-	P	C	-	G	S	G	T	F	T	S	R	N	N	T	S	R	N	N		
59	K	T	N	T	-	T	N	T	-	Q	C	-	P	C	-	A	S	D	T	F	T	S	R	N	N	T	A	S	N	N		
60	K	T	N	T	-	T	N	T	-	Q	C	-	P	C	-	T	E	G	V	D	Y	T	N	A	S	N	N	E	P	S		
58	S	-	E	H	T	G	A	C	N	-	P	C	T	-	P	C	T	F	P	C	T	V	-	C	K	S	D	-	T	N	F	R
60	S	-	E	H	T	G	A	C	N	-	P	C	T	-	P	C	T	F	P	C	T	V	-	C	K	S	D	-	T	N	F	R

FIG. 2C

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FIG. 2D

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FIG. 2E

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		Consensus #1
178	E C V S C S N C K - - - - -	- - - - - K S L E C T K L C L P - - - - -
178	I C R P H Q I C N V V A - - - - -	- - - - - I P G N A S R D A V C T S T S P T R S M A P - - - - -
163	P C L P C T V C E D T E R Q - L R E C T R W A D A E C - - E E I P G R W I T R S N G F R	- - - - - E E I P G R W I T R S N G F R
186	R C Q P H T R C E I Q G L V E A A P G T S Y S D T I C K N P P E P G A M L L - - - - -	- - - - - E E I P G R W I T R S N G F R
142	H C D P C T K C E - - - - -	- - - - - E E I P G R W I T R S N G F R
111	Q C R D - K E C T - - - - -	- - - - - E E I P G R W I T R S N G F R
165	N C K E P S S G T I P Q - A K P T P V S P A T S S A S T M P V R G G T R L A Q E C D 3 0	- - - - - E E I P G R W I T R S N G F R
160	K C H P W T S C E T K D L V V Q Q A G T N K T D V V C - - - G P Q D R L R - - C D 4 0	- - - - - E E I P G R W I T R S N G F R
133	- C R P W T N C S L D G K S V L V N G T K E R D V V C G P S P - - - - - A 4-1 B B	- - - - - E E I P G R W I T R S N G F R
140	A C K P W T N C T L A G K H T L Q P A S N S S D A I C - - E D - - - - - O X 4 0	- - - - - E E I P G R W I T R S N G F R
167	K C E P V P N N T F N Y I D V E I T L Y P V N D T S C T R T T T - - - - - V C 2 2	- - - - - E E I P G R W I T R S N G F R
167	K C E P V P S N T F N Y I D V E I N L Y P V N D T S C T R T T T - - - - - C R M B	- - - - - E E I P G R W I T R S N G F R
140	N C T S - - - W - - - - -	- - - - - D D I Q C V E E - - - - - T N F R - l i k e

FIG. 2F

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		Consensus #1
198	- - - - - Q I E N V K G T E D S G T T V L L P L V I F F G - L - - - - -	TNFR1
212	- - - - - G A V H L P Q P V S T R S Q H T Q P T P E P S T A P S T S F L L P M G P S P P A	TNFR2
200	- - - - - T P P E G S D S T A P S T Q E P E A P P E Q D L I A S T - - - - -	NGFR
224	- - - - - L A I L S - - - - -	LTOR
159	- - - - - L T S N T K C K E G S R S N L - - - - -	GWL
130	- - A R S S Q A L S P H P Q P T H L P Y V S E M L E A R - - - - -	FAS
204	- - A A S K L T R A P D S P S S V G R P S S D P G L S P T Q P - - - - -	CD27
194	- - A L V V I P - - - - -	CD30
164	- - D L S P G A S S V T P P A P A R E P G H S P Q I S - - - - -	CD40
169	- - - - - R D P P A T Q P Q E T Q G P P - - - - -	4-1BB
200	- - - - - G L S E S I L T - - - - -	OX40
200	- - - - - G L S E S I S T - - - - -	VC22
153	- - - - - F G - - - - -	TNFR-like

FIG. 2G

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		Consensus #1
223	-	-
252	E G S T G D F A L	- C L L S I L F I G L M Y - - - - -
236	M G S S Q P V V T R G T T D N L I P V Y C S I L A A V V V G L V A - - - - -	- P V G L I V G V T A L G L L I I G V V TNFR2
230	-	- V L F I L L F T T V L A C A W M R H P S LTOR
178	-	- C L L - L L P I P L I V - - - - -
164	A D	- - - - -
242	K Q C E P D Y Y L D E A G R C T A C V S C S R D	- D L V E K T P C A W N S S R T C
200	-	- I F G I L F A I L L V L V F I K K - - - - -
190	-	- F F L - - - - -
184	-	- A R P I T V Q P T E A - - - - -
221	P V F R E E Y	- - - - - F S V L N K V A T S G F F T G E N R
221	P V F R N G Y	- - - - - F S V L N E V A T S G F F T G Q N R
155	-	- - - - - CRMB

FIG. 2H

		Consensus #1
235	- - - R Y Q R W - K S K L Y S I - - -	- V C G K S T P E K E G E L E G T T
280	N C V - - I M T Q V K K P L C - - -	T N F R L
269	- - - Y I A F K R W N S C K Q - - -	T N F R 2
250	L C R - - K L G T L L K R H - - -	N G F R
189	- - - W V K R K E V Q K - - -	L T O R
166	- - - F R Q - - -	F A S
282	E C R P G M I C A T S A T N S C A R C V P Y P I C A A E T V T K P Q D M A E K D	C D 27
218	- - - V A K K - - -	C D 30
193	- - - W P - - R - - -	C D 40
195	- - - Y Q N I S K - - V C T - - -	4-1FB
246	- - - Y Q N I S K - - V C T - - -	O X 40
246	- - - A N A T V E T P A A E E T M N	V C 22
155	- - - C R M B	T N F R - l i k e

FIG.21

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		Consensus #1
264	T K P L A P N P S F S P T P G F T P T L G F S P V P S S T F T S S T Y T P G D	TNFR1
294	- - - L Q R E A K V P H L P A - D K A R G T Q G P E Q Q H L L I T A -	TNFR2
281	- - - - - N K Q G A N S R P V - N Q T P P P E G E K L H S D S G I S V D	NGFR
262	- - - - - P E G E E S P P C P A - P R A D P H F P D L A E P L L -	LTFR
212	- - - S P T L N P E - - T V A I N L S D V D L S K Y I T T -	FAS
169	- - - - - P T N K A P H P K Q E - P Q - E I N F P D -	CD27
322	T T F E A P P L G T Q P D C N P T P E - N G E A P A S T S P T Q S L L V D S Q A	CD30
222	- - - - - P T N K A P H P K Q E - P Q - E I N F P D -	CD40
193	- - - - - T S Q G P S T R P V - E - - V P G G R A V A A I L G L G L -	4-1BB
198	- - - - - T S Q G P S T R P V - E - - V P G G R A V A A I L G L G L -	OK40
255	- - - - - L N F E I K C N N - - - - K G S - - S F K Q - - L T K -	VC22
255	- - - - - L N F E I K C N N - - - - K D S Y S S S K Q - - L T K -	CRMB
170	T S P G T P A P A E E T M N T S P G T P A P A E E T M T T S P G T - - -	TNFR-like

FIG. 2J

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		Consensus #1
304	C P N F A A P R R E V A P P Y Q G A D P I L A T A	- - - - -
324	- - - P S	- - - - -
311	S Q S L H D Q Q P H T Q T A S G Q A L K	- - - G D G G L Y S S L P P A K R E E
288	- - - P M S G D L S P S P A G P P T	- - - I I T Q R
236	- - - - -	- - - FAS
171	A R T L S T H W P P Q R S L C S S D F I	- - - R I L V I F S G M F L V F T L A
361	S K T L P I P T S A P V A L S S T G K P V L D A G P V L F W V I L V L V V V G	CD27
241	- - - - - D L P G S N T A A P V	CD30
193	- - - - - A L T S T A L L F L	- - - - -
224	- - - - - V I L G L L	- - - L F F L T L R F S V V K R
274	- - - A K N D D G - M	4-1B
276	- - - T K N D D D S I	- - - - -
205	- - - P A P A A E E T M T T S	- - - - - CRMB
		- - - - - TNFR-like

FIG. 2K

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		Consensus #1
329	- - -	L A S D P I P N P L Q K W E D S A H K P Q S L D T D D P A T L Y A V V E
339	- - -	- - - D R R A P T R N Q P Q A P G V E A S G A G E A R A S T G S S D S S
347	V E K L	- - - - - Q S P L - - - - - V Q A R E L - - E A E L I I R
303	- - -	- - - A P S L E E V V L Q Q S P L - - - - -
240	- - -	- - - M T L S Q V - - - - -
207	G A L F L	- - - - -
401	S S A F L L	U C H R R A C R K R I R Q K L H L C Y P V Q T S Q P K L E L V D S R P
252	- - -	- - - - - Q E T L - - - - -
216	G R K K L	- - - - -
245	- - -	- - - - -
281	- - -	- - - M S H S E T V T L A G D C L S S V D I Y I L Y S N T N V C 22
284	- - -	- - - M P H S E S V T L V G D C L S S V D I Y I L Y S N T N C R M B
217	- - -	- - - P G T P A P A E E T M T S P G T P A S - - - - -

FIG.2L

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		Consensus #1
365	N V P P L R W K E F V R R L G L S D	D H E I D R L E L Q N G R C L R E A Q Y S M L
372	P G G H G T Q V N V T C I V N V C S S S D H	- S S Q C S S Q A S S T M G D T -
355	A G D T W R H L A G E L G Y Q P E H I D S F T H E A C	- - - - - A L L
327	P G E H G Q V A H G A N G I H V T G G S V T V T G N I Y I Y N G P V L G G T -	- LTR
246	- - - - - K G F V R K N G V N E A K I D E I K N D N V Q D T A E Q K V Q L L	FAS
214	- - - R R K Y R S N K G E S P V E P A E P C R Y S C	- - - - - CD27
441	R R S S T Q L R S G A S V T E P V A E E R G L M S Q P L M E T C H S V G A A Y L	CD30
256	- - - - - H G C Q P V T -	- - - - - CD40
222	- - - - - - - - -	- - - - - 4-1EB
245	- - - R L P P D - A H K P P G G S E -	- - - - - OX40
308	A Q D Y E T D T I S Y R V G N V L D D D S H M P G S C N I H K -	- - - - - VC22
311	T Q D Y E T D T I S Y H V G N V L D V D S H M P G R C D T H K -	- - - - - CRMB
238	- - - - -	- - - - - TNFR-like

FIG. 2M

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		Consensus #1
405	A T W R R T P R R E A T L E L L G R V L R D M D L L G C - - - - -	- - - - -
409	- - - D S S P S E S - P K D E - - - Q V P F S K E E C A F - - - - -	- - - - -
388	A S W A T Q D S A T L D A - - - - -	- - - - -
365	- - - R G P G D P - P A P P - - - E P P Y P T P E E G A - - - - -	- - - - -
279	R N W H Q L H G K K E A - Y D T L I K D L K K A N L - - C T L A E K I Q - - - - -	- - - - -
239	- - E E E G S T I - - - - -	- - - - -
481	E S I L P L Q D A S P A G G - P S S P R D L P E P R V S T E H T N N K I E K I Y I	CD30
263	- - - - -	CD40
222	- - - - -	- - - - -
260	- - - - -	QX40
339	- - - - -	- - - - -
342	- - - - -	VC22
238	- - - - -	CRMB
	- - S H Y L S C T I V G I I V - - - - -	TNFR-like

FIG. 2N

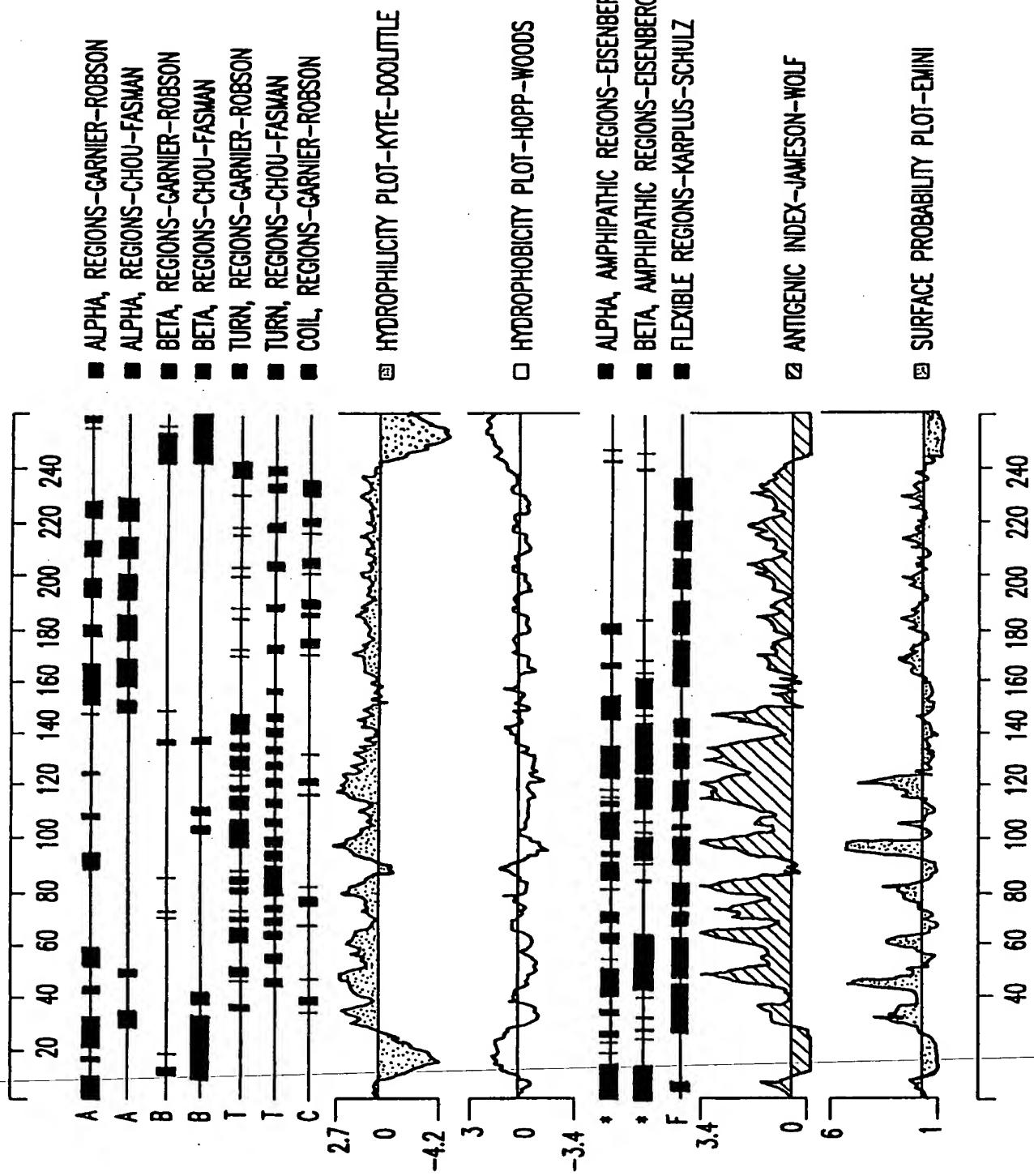
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FIG. 20

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FIG. 2 P

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Appl. No. To be assigned; Group Art Unit: To be assigned
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 Inventors: Wei *et al.*; Tel: 202/371-2600
 Title: Tumor Necrosis Factor Receptor 5

HPRCB54R

1 GAATTCGGCA NAGCCTCTCC ACGCGCACGA ACTCAGCCAA CGATTTCTGA
 51 TAGATTTTG GGAGTTTGAC CAGAGATGCA AGGGGTGAAG GAGCGCTTCC
 101 TACCGTTAGG AACTCTGGGG ACAGNNCGCC CCGGCCGCCT GATGGCCGAG
 151 GCAGGGTGC G ACCCAGGACC CAGGACGGCG TCGGGAACCA TACCATGGCC
 201 CGGATCCCCA AGACCCCTAAA GTTCGTGGTC GTCATCGTCG CGGTCTGCT
 251 GCCAGTCCTA GCTTA C TCTG CCACCA CTGC CCGGCAGAGG AAGTTNCCA
 301 GCAGNCANTG GNCCCACAGC AACAGNGGCA CAGTTCAAG GGGGNAGGAG
 351 TTTTCCANCA AGTTTTATA GTTCAGAACN TATTGGNGCT NTNAACCCTT
 401 GCACAAGGGT TTGGNTTAAA CCAANGTTTC CAANATGNAC TTTTNGTTC
 451 CCTGTTANAT TTTTAATTAA GTTNAANNTT AAATTTNTNA ACCTTNCCNG
 501 GGNAAATT

HSJAU57RA

1 GGCAGAGGGT TCTCCAGCCT GGCTCTATCT TCCTCCTTGT NATCGTCCA
 51 TCCCCACATC CCGTGCACCC CCCAGGACCC TGGTCTCATC AGTCCCTCTC
 101 CTGGAGCTGG GGGTCCACAC ATCTCCCAGC CAAGTCCAAG AGGGCAGGGC
 151 CAGTTCCCTCC CATCTTCAGG CCCAGCCAGG CAGGGGGCAG TCGGCTCCTC
 201 AACTGGGTGA CAAGGGTGAG GATGAGAAGT GGTCACGGGG ATTATTACAG
 251 CCTTGGTCAG AGCAGAACAC AGAGTTTTTC CGTGTGTTGG TTTTACTCT
 301 NNTTCCCTT CTTNATNCC CTTTCN

HUSCB54R

1 CCAGGGTCTC CTNCCCCACC TGCTGAAGAG ACANTGACCA CCAGCCCGGG
 51 GACTCCTGCC TCTTCCTCAT TACCTCTNAT GNANCATCGT AGGGATCATA
 101 GTTCTAATTG TGCCCTCTGA ATTGTGCTTT GTTTGGAAAG ACTTCACTGT
 151 GGGAAAGAAAT TCCTTCCTTA CCTGAAGTTG CAGGTAGGCC CTGGGTNAGG
 201 GCGNGGGCGC CTGGACANTN TCTGGNCCTG GCTGCCCGCT G

HELBP70R

1 GGCAGAGGCC CCAGCTGCTG AAGAGACAAT AATCACCAGC CCGGGGACTC
 51 CTGNNTCTNC TNATTACCTC TNATGCACCA TCGTAGGGAT CATAGTTCTA
 101 ATTGTGCCCT CTAATTGTTT TTGTTGAAA AGANTTCACT GTGGAAGAAA
 151 TTCCCTCCTT ACCTGTAAGT TNCAGGTAGG NGCCTGGCTG AGGGCGGGGG
 201 GCGCTGGTAC ACTCTCTGAC CCTGCCTCCC TCTGNCTGTT TTCCCACAGA
 251 CAGAAACGCC TGCCCCCTGNC CCCAAGTTCC TNGTGTTC CAGCCTGGCT
 301 CTATCTTNNC TCCTTGTGAA TCGTTCCCAT CCCCACANGC

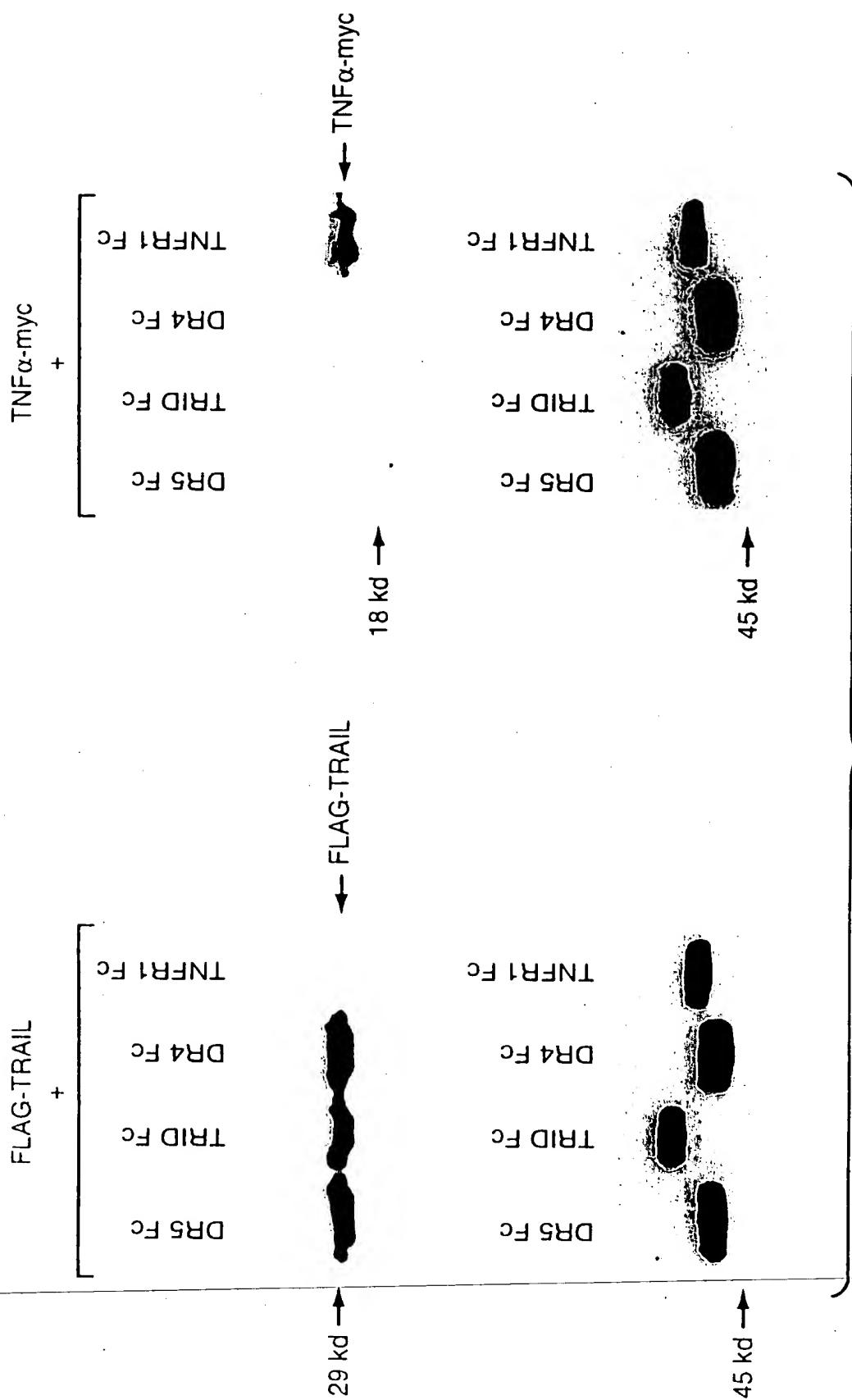


FIG. 5A

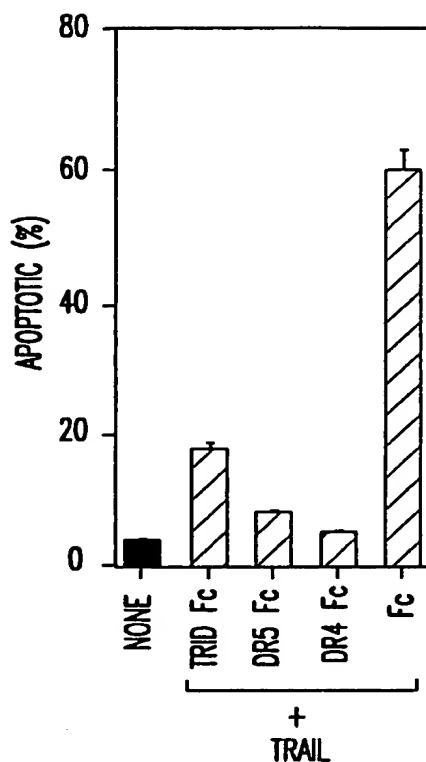


FIG.5B

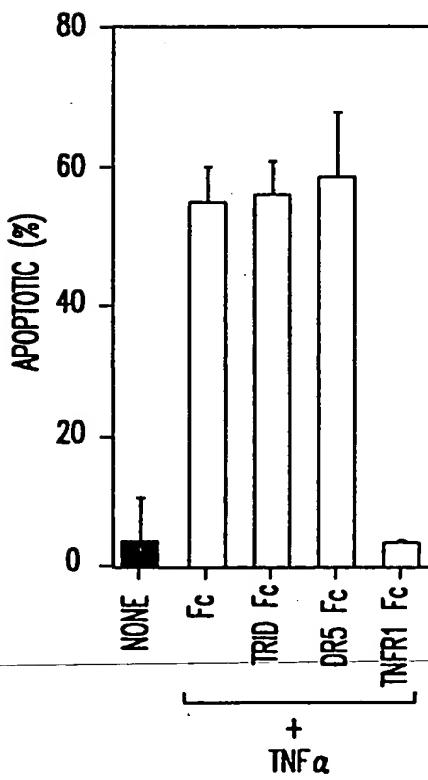


FIG.5C

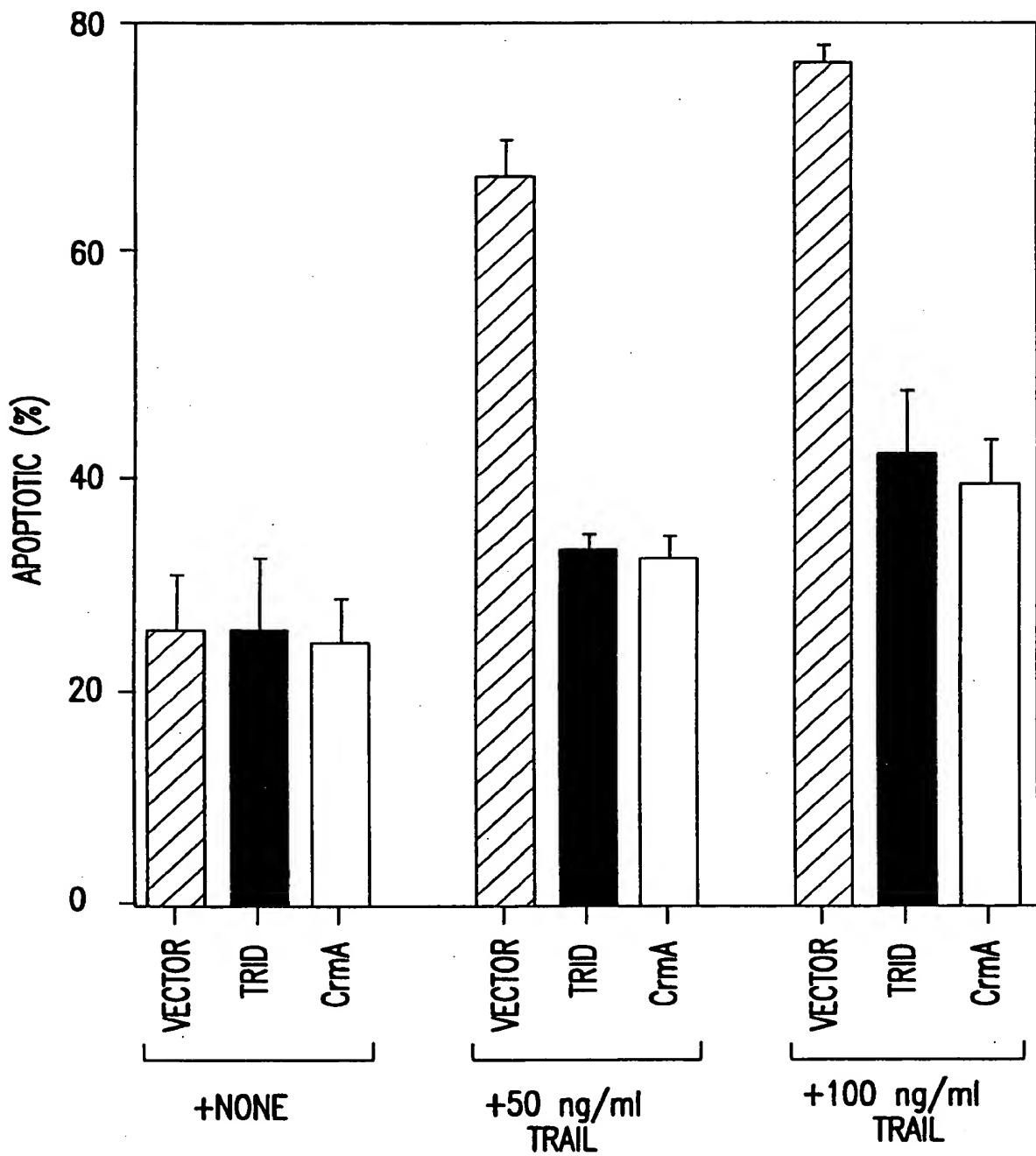


FIG. 6